1

SEQUENCE LISTING

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<150> US 60/496,188

<151> 2003-08-18

<160> 96

<170> PatentIn version 3.2

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile 35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys 50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp 65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val 85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr 130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val 145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr 165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met 195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys 210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu 225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile 245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe 260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser 275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp 290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys 305 310 315 320

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Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val 340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile 355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile 370 375 380

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Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly 405 410 415

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Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala 435 440 445

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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr

330

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Ile 385	Glu	Asp	Ser	Leu	Leu 390	Met	Gly	Ala	Asp	Tyr 395	Tyr	Glu	Thr	Glu	Ala 400
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys 50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile 65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr 85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
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Tyr	Glu	Lys	Phe 180	Ile	Gln	Ala	His	Arg 185	Glu	Thr	Asn	Ala	Asp 190	Ile	Thr
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
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Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
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Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn 145 150 155 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp 165 170 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr 180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu 195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro 210 215 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly 225 230 235 240

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11

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- Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile 325 330 335
- Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp 340 345 350
- Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys 355 360 365
- Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala 370 375 380
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aatgctgaca	atgttcaaga	agctgcaatg	gagacagacg	ggtacttcat	caaaggtgga	1380
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<210> 10

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn 20 25 30

Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly 35 40 45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys 50 55 60

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Ala	Tyr	Gly 115	Ser	Asn	Ile	Gly	Gly 120	Tyr	Ъуs	Asn	Glu	Gly 125	Phe	Val	Glu
Val	Leu 130	Ala	Ala	Gln	Gln	Ser 135	Pro	Asp	Asn	Pro	Asn 140	Trp	Phe	Gln	Gly
Thr 145	Ala	Asp	Ala	Val	Arg 150	Gln	Tyr	Leu	Trp	Leu 155	Phe	Glu	Glu	His	Asn 160
Val	Met	Glu	Phe	Leu 165	Ile	Leu	Ala	Gly	Asp 170	His	Leu	Tyr	Arg	Met 175	Asp
Tyr	Glu	ГÀЗ	Phe 180	Ile	Gln	Ala	His	Arg 185	Glu	Thr	Asn	Ala	Asp 190	Ile	Thr
Val	Ala	Ala 195	Leu	Pro	Met	Asp	Glu 200	Lys	Arg	Ala	Thr	Ala 205	Phe	Gly	Leu
Met	Lys 210	Ile	Asp	Glu	Glu	Gly 215	Arg	Ile	Ile	Glu	Phe 220	Ala	Glu	Lys	Pro
Lys 225	Gly	Glu	Gln	Leu	Lys 230	Ala	Met	Met	Val	Asp 235	Thr	Thr	Ile	Leu	Gly 240
Leu	Asp	Asp	Val	Arg 245	Ala	Lys	Glu	Met	Pro 250	Tyr	Ile	Ala	Ser	Met 255	Gly
Ile	Tyr	Val	Phe 260	Ser	Lys	Asp	Val	Met 265	Leu	Gln	Leu	Leu	Arg 270	Glu	Gln
Phe	Pro	Glu 275	Ala	Asn	Asp	Phe	Gly 280	Ser	Glu	Val	Ile	Pro 285	Gly	Ala	Thr
Ser	Ile 290	Gly	Lys	Arg	Val	Gln 295	Ala	Tyr	Leu	Tyr	Asp 300	Gly	Tyr	Trp	Glu
Asp 305	Ile	Gly	Thr	Ile	Ala 310	Ala	Phe	Tyr	Asn	Ala 315		Leu	Gly	Ile	Thr 320
Lys	Lys	Pro	Ile	Pro 325		Phe	Ser	Phe	Tyr 330		Arg	Phe	Ala	Pro 335	Ile
Tyr	Thr	Gln	Pro 340	Arg	His	Leu	Pro	Pro 345	Ser	ГÀЗ	Val	Leu	Asp 350	Ala	Asp
Val	Thr	Asp 355		Val	Ile	Gly	Glu 360		Cys	Val	Ile	ьуs 365		СЛа	Lys
Ile	Asn 370		Ser	Val	Val	Gly 375	Leu	Arg	Ser	Сув	Ile 380		Glu	Gly	Ala
Ile 385		Glu	Asp	Ser	Leu 390		Met	Gly	Ala	Asp 395		Tyr	Glu	Thr	Glu 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile 410 405 Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg 425 Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala 440 Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val 460 455 Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile <210> 11 <211> 1582 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (1368) <223> r = a or g; amino acid 453 = Pro. <221> variation <222> (1578) <223> k = g or t.<400> 11 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat

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Cys	Pro	Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	
				cgt Arg												291
				cct Pro												339
				tac Tyr 115												387
				aat Asn												435
				cat His												483
ttt Phe	gct Ala 160	gat Asp	gga Gly	tct Ser	gta Val	cag Gln 165	gta Val	tta Leu	gcg Ala	gct Ala	aca Thr 170	caa Gln	atg Met	cct Pro	gaa Glu	531
gag Glu 175	cca Pro	gct Ala	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
				ggc										Glu		6,75
	Gln		His	gtc Val	Glu	Asp	Asp	Ala	Asp	Ile		Ile	Ser		gct Ala	723
cct Pro	gtt Val 240	Asp	gag Glu	ago Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	gly	cta Leu 250	. Val	aag Lys	att Ile	gat Asp	771
cat His 255	Thr	gga Gly	. cgt . Arg	gta Val	ctt Leu 260	Glr	tto Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Lev	aat Asn	tct Ser	atg Met	aga Arg 275	y Val	gag Glu	g acc 1 Thr	aac Asn	tto Phe 280	. Lev	g ago L Ser	tat Tyr	gct Ala	ata Ile 285	gat Asp	867
gat Asp	gca Ala	cag Gln	aaa Lys 290	Tyr	cca Pro	tac Tyr	ctt Lev	gca Ala 295	Ser	atg Met	g ggc	att Ile	tate Tyr	. Val	ttc Phe	915

16

aag Lys	aaa Lys	gat Asp 305	gca Ala	ctt Leu	tta Leu	gac Asp	ctt Leu 310	ctc Leu	aag Lys	tca Ser	aaa Lys	tat Tyr 315	act Thr	caa Gln	tta Leu	963
cat His	gac Asp 320	ttt Phe	gga Gly	tct Ser	gaa Glu	atc Ile 325	ctc Leu	cca Pro	aga Arg	gct Ala	gta Val 330	cta Leu	gat Asp	cat His	agt Seŕ	1011
gtg Val 335	cag Gln	gca Ala	tgc Cys	att Ile	ttt Phe 340	acg Thr	ggc	tat Tyr	tgg Trp	gag Glu 345	gat Asp	gtt Val	gga Gly	aca Thr	atc Ile 350	1059
aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
												gca Ala				1155
ttg Leu	cct Pro	ccg Pro 385	acg Thr	caa Gln	ttg Leu	gac Asp	aag Lys 390	tgc Cys	aag Lys	atg Met	aaa Lys	tat Tyr 395	gca Ala	ttt Phe	atc Ile	1203
tca Ser	gat Asp 400	ggt Gly	tgc Cys	tta Leu	ctg Leu	aga Arg 405	gaa Glu	tgc Cys	aac Asn	atc Ile	gag Glu 410	cat His	tct Ser	gtg Val	att Ile	1251
gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
atg Met	atg Met	gga Gly	gcg Ala	gac Asp 435	Ile	tat Tyr	gaa Glu	act Thr	gaa Glu 440	Glu	gaa Glu	gct Ala	tca Ser	aag Lys 445	cta Leu	1347
ctg Leu	tta Leu	gct Ala	ggg Gly 450	Lys	gtc Val	ccr Pro	gtt Val	gga Gly 455	Ile	gga Gly	agg Arg	aac Asn	aca Thr 460	. PAs	ata Ile	1395
agg Arg	aac Asn	tgt Cys 465	Ile	att Ile	gac Asp	atg Met	aat Asn 470	Ala	agg Arg	ı att ı Ile	ggs Gly	y aag y Lys 475	Asn	gtg Val	gtg Val	1443
ato Ile	aca Thr 480	Asr	agt Ser	aag Lys	gly ggc	atc Ile 485	Glr	gag Glu	gct Ala	gat Asp	Cac His 490	Pro	gaa Glu	ı gaa ı Glu	. Gly	1491
tac Tyr 495	Ser	tac Tyr	tac Tyr	ata Ile	agg Arg 500	ser,	gga Gly	ato Ile	gto Val	g gtg L Val 505	I I l	c cto e Lev	ı aaçı Lys	g aat S Asr	gca Ala 510	1539
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17

<212> PRT

<213> Zea mays

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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 330

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 395 390

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 410 405

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 470

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Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 505

Asn Asp Gly Ser Val Ile 515

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<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

<221> variation

<222> (267) <223> k = g or t; amino acid 86 = Ala. <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1368) <223> r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.<400> 13 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu 20 15 agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe 35 40 ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala 50 55 tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 70 291 get gat gea aac egt gta tet gek ate att ttg gge gga gge act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 105 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 120 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn 150

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												tac Tyr				675
gtg Val	cag Gln	aaa Lys 225	cat His	gtc Val	gag Glu	gac Asp	gat Asp 230	gct Ala	gat Asp	atc Ile	act Thr	ata Ile 235	tca Ser	tgt Cys	gct Ala	723
												gtg Val				771
cat His 255	act Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	cca Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	gtt Val	gag Glu	acc Thr	aac Asn	ttc Phe 280	ctg Leu	agc Ser	tat Tyr	gct Ala	ata Ile 285	gat Asp	867
gat Asp	gca Ala	cag Gln	aaa Lys 290	tat Tyr	cca Pro	tac Tyr	ctt Leu	gca Ala 295	Ser	atg Met	ggc	att Ile	tat Tyr 300	gtc Val	ttc Phe	915
			Ala					Leu					Thr		tta Leu	963
cat His	gac Asp 320	Phe	gga Gly	tct Ser	gaa Glu	ato Ile 325	Leu	cca Pro	aga Arg	gct Ala	gta Val 330	Leu	gat Asp	tay Tyr	agt Ser	1011
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tto Lei	g cct ı Pro	cco Pro	g acc	g caa Glr	tto Lev	g gad L Asp	aag Lys	g tgo s Cys	c aag s Lys	g ato Met	g aaa Lys	a tat g Tyr	gca Ala	ttt a Phe	atc lle	1203

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gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	agc Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	ctc Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
atg Met	atg Met	gga Gly	gcg Ala	gac Asp 435	atc Ile	tat Tyr	gaa Glu	Thr	gaa Glu 440	gaa Glu	gaa Glu	gct Ala	tca Ser	aag Lys 445	cta Leu	1347
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							aat Asn 470									1443
atc Ile	aca Thr 480	aac Asn	agt Ser	aag Lys	ggc	atc Ile 485	caa Gln	gag Glu	gct Ala	gat Asp	cac His 490	ccg Pro	gaa Glu	gaa Glu	gjå aaa	1491
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Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly 105 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 120 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 185 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 200 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 215 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 235 230 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 265 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 , 280 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 365 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val

23

405 410 415 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 470 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 505 Asn Asp Gly Ser Val Ile 515 <210> 15 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1368) $\langle 223 \rangle$ r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.<400> 15 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His 10

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15	TTE	Arg	ser	Cys	20 20	стλ	Asp	GIĀ	TTE	Asp 25	Arg	ьеи	GIU	пув	30	
											aga Arg					147
											ctt Leu					195
											tct Ser					243
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp 80	Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	
											acg Thr					339
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											gaa Glu					483
											aca Thr 170	Gln			gaa Glu	531
gag Glu 175	Pro	gct Ala	gga Gly	tgg Trp	ttc Phe 180	Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
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gta Val	atc Ile	ttg Leu	agt Ser 210	Gly	gat Asp	cag Gln	ctt Leu	tat Tyr 215	Arg	atg Met	aat Asn	tac Tyr	atg Met 220	Glu	ctt Leu	675
gtg Val	cag Gln	aaa Lys 225	His	gto Val	gag Glu	gac Asp	gat Asp 230) Ala	gat Asp	ato	act Thr	ata Ile 235	Ser	tgt Cys	gct Ala	723
cct	gtt	gat	gag	ago	cga	gct	tct	aaa	aat	ggg	g cta	gtg	aag	att	gat	771

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Pro	Val 240	Asp	Glu	Ser	Arg	Ala 245	Ser	Lys	Asn	Gly	Leu 250	Val	ГÀз	Ile	Asp	
cat His 255	act Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	cca Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	gtt Val	gag Glu	acc Thr	aac Asn	ttc Phe 280	ctg Leu	agc Ser	tat Tyr	gct Ala	ata Ile 285	gat Asp	867
gat Asp	gca Ala	cag Gln	aaa Lys 290	tat Tyr	cca Pro	tac Tyr	ctt Leu	gca Ala 295	tca Ser	atg Met	ggc Gly	att Ile	tat Tyr 300	gtc Val	ttc Phe	915
aag Lys	aaa Lys	gat Asp 305	gca Ala	ctt Leu	tta Leu	gac Asp	ctt Leu 310	ctc Leu	aag Lys	tca Ser	aaa Lys	tat Tyr 315	act Thr	caa Gln	tta Leu	963
cat His	gac Asp 320	ttt Phe	gga Gly	tct Ser	gaa Glu	atc Ile 325	ctc Leu	cca Pro	aga Arg	gct Ala	gta Val 330	cta Leu	gat Asp	tay Tyr	agt Ser	1011
gtg Val 335	Gln	gca Ala	tgc Cys	att Ile	ttt Phe 340	acg Thr	ggc	tat Tyr	tgg Trp	gag Glu 345	gat Asp	gtt Val	gga Gly	aca Thr	atc Ile 350	1059
aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
ttt Phe	gat Asp	ttt Phe	tac Tyr 370	Asp	cca Pro	aaa Lys	aca Thr	cct Pro 375	Phe	ttc Phe	act Thr	gca Ala	ccc Pro 380	Arg	tgc Cys	1155
tt <u>e</u> Lev	g cct L Pro	ccg Pro 385	acg Thr	caa Gln	ttg Leu	gac Asp	aag Lys 390	Cys	aag Lys	atg Met	aaa Lys	tat Tyr 395	Ala	ttt Phe	atc Ile	1203
Ser	: Asp	Gly	tgc Cys	Leu	Leu	Arg	Glu	ı Cys	Asn	Ile	gag Glu 410	His	tct Ser	gtg Val	att Ile	1251
998 Gly 415	/ Val	tgo Cys	tca Ser	cgt Arg	gto Val 420	Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	ı Lev	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
at <u>e</u> Met	g atg : Met	gga Gly	a gcg / Ala	gac Asp 435	Ile	tat Tyr	gaa Glu	a act 1 Thr	gaa Glu 440	Glu	a gaa a Glu	ı gct ı Ala	tca Ser	aag Lys 445	cta Leu	1347
cto Lev	g tta ı Lev	a gct 1 Ala	= 999 a Gly 450	, PA	g gto Val	ccr Pro	gtt Val	gga L Gl _y 455	/ Ile	gga gga	a ago / Aro	g aac g Asr	aca Thi 460	: Гу	g ata s Ile	1395
agg Arg	g aad g Asr	tgi 1 Cys 46	s Ile	c att	gad Bag	ato Met	aat Asi 470	n Ala	agg Arg	g att	e Gly	g aag 7 Lys 475	: Ası	gtg n Val	g gtg L Val	1443

				caa Gln							1491
				gtg Val							1539
gat Asp		_	taga	atcgg	get g	gcgt}	ctgc <u>s</u>	ā			1576

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<212> PRT

<213> Zea mays

<400> 16

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

Leu	Ser 210	Gly	Asp	Gln	Leu	Tyr 215	Arg	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Ьуз 225	His	Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235	Ser	Cys	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245	Ser	Lys	Asn	Gly	Leu 250	val	ГÀв	Ile	qaA	His 255	Thr
Gly	Arg	Val	Leu 260	Gln	Phe	Phe	Glu	Lys 265	Pro	Lys	Gly	Ala	Asp 270	Leu	Asn
Ser	Met	Arg 275	Val	Glu	Thr	Asn	Phe 280	Leu	Ser	Tyr	Ala	Ile 285	Asp	Asp	Ala
Gln	Lys 290	Tyr	Pro	Tyr	Leu	Ala 295	Ser	Met	Gly	Ile	Tyr 300	Val	Phe	Lys	Lys
Asp 305	Ala	Leu	Leu	Asp	Leu 310	Leu	Lys	Ser	Lys	Туr 315	Thr	Gln	Leu	His	Asp 320
Phe	Gly	Ser	Glu	Ile 325	Leu	Pro	Arg	Ala	Val 330	Leu	Asp	Tyr	Ser	Val 335	Gln
Ala	Сув	Ile	Phe 340	Thr	Gly	Tyr	Trp	Glu 345	Asp	Val	Gly	Thr	Ile 350	Lys	Ser
Phe	Phe	Asp 355		Asn	Leu	Ala	Leu 360	Thr	Glu	Gln	Pro	Ser 365	Lys	Phe	Asp
Phe	Туr 370		Pro	Lys	Thr	Pro 375		Phe	Thr	Ala	Pro 380	Arg	Сув	Leu	Pro
Pro 385		Gln	Leu	Asp	Lys 390		Lys	Met	Lys	Tyr 395		Phe	Ile	Ser	Asp 400
Gly	Cys	Leu	Leu	Arg 405		Сув	Asn	Ile	Glu 410		Ser	· Val	Ile	Gly 415	۷al
Сўз	Ser	Arg	Val 420		Ser	Gly	Cys	Glu 425		Lys	Asp	Ser	Val 430	Met	Met
Gly	Ala	Asp 435		Туг	Glu	Thr	Glu 440		Glu	. Ala	Ser	Lys 445		Leu	Let
Ala	Gly 450		Val	Pro	Val	Gly 455		Gly	Arg	, Asn	Thr 460	. Lys	Ile	Arg	Ası
Cys 465		: Ile	a Asp	Met	470		a Arg	Ile	gly	475		ı Val	. Val	Ile	Th:
Asn	ser	. PAS	Gly	11e 485		Glu	ı Ala	Asp	490		Glu	ı Glü	Gly	Tyr 495	
Ile	arg	ser,	Gly 500		val	. Val	. Il∈	ь Lev 505		s Asr	a Ala	a Thr	510		Ası
Gly	, Ser	. Val	. Ile	:											

515

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<210> 17
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<212> DNA
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<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable
<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.
<220>
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<222> (1008)
<223> y = c or t.
<220>
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<222> (1368)
<223> r = a \text{ or } g; \text{ amino acid } 453 = Pro.
<220>
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<222> (1578)
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65
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gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp 08	Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	
	_				_				_	_	acg Thr		_			339
											atg Met					387
											cag Gln					435
											gaa Glu					483
	-	-			_	_	_				aca Thr 170					531
											tct Ser					579
											tcc Ser					627
									Arg		aat Asn			Glu		675
								Ala			act Thr		Ser			723
cct Pro	gtt Val 240	Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	gly	cta Leu 250	gtg Val	aag Lys	att Ile	gat Asp	771
	Thr					Gln					Pro				gat Asp 270	819
					Val					Leu					gat Asp	867
				Tyr					Ser					· Val	ttc Phe	915
aag Lys	aaa Lys	gat Asp	gca Ala	. ctt . Leu	tta Leu	gac Asp	ctt Leu	cto Lev	aag Lys	tca Ser	aaa Lys	tat Tyr	act Thr	caa Glr	tta Leu	963

		305					310					315				
												cta : Leu				1011
												gtt Val				1059
aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
												gca Ala				1155
												tat Tyr 395				1203
tca Ser	gat Asp 400	ggt Gly	tgc Cys	tta Leu	ctg Leu	aga Arg 405	gaa Glu	tgc Cys	aac Asn	atc Ile	gag Glu 410	cat His	tct Ser	gtg Val	att Ile	1251
												aag Lys				1299
												gct Ala				1347
															ata Ile,	1395
								Ala				aag Lys 475			gtg Val	1443
atc Ile	aca Thr 480	Asn	agt Ser	aag Lys	ggc	atc Ile 485	caa Gln	gag Glu	gct Ala	gat Asp	cac His 490	Pro	gaa Glu	gaa Glu	ej aaa	1491
tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	atc Ile	ctg Leu 505	. Lys	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
			tct Ser		Ile		atcg	gct	gcgt	ktgc	g					1576

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<211> 516

<212> PRT

<213> Zea mays

<400> 18

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270

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Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

32

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<222> (1008)
<223> y = c or t.
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<222> (1209)
<223> y = c or t.
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<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
<221> variation
<222> (1371)
<223> h = a or c or t/u.
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<223> k = g or t.
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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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                                      40
                                                                    195
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                                  55
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                     243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
                              70
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                     291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80
tet cag etc ttt ect etg aca age aca aga get acg ect get gta ect,
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
                                                              110
 95
                     100
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                 115
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34

			ata Ile 130													435 ·
			cgc Arg													483
			gga Gly													531
			gga Gly													579
			ctc Leu													627
			agt Ser 210													675
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			gag Glu									Val				771
			cgt Arg													819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	gtt Val	gag Glu	acc Thr	aac Asn	ttc Phe 280	ctg Leu	agc Ser	tat Tyr	gct Ala	ata Ile 285	Asp	867
			aaa Lys 290						Ser					Val	ttc Phe	915
aag Lys	aaa Lys	gat Asp 305	Ala	ctt Leu	tta Leu	gac Asp	Leu 310	Leu	aag Lys	tca Ser	aaa Lys	tat Tyr 315	Thr	caa Gln	tta Leu	963 ·
cat His	gac Asp 320	Phe	gga Gly	tct Ser	gaa Glu	ato Ile 325	Leu	cca Pro	aga Arg	gct Ala	gta Val 330	. Leu	gat Asp	cay His	agt Ser	1011
gtg Val 335	Gln	gca Ala	tgc Cys	att Ile	ttt Phe 340	Thr	Gly	tat Tyr	tgg Trp	gag Glu 345	ı Asp	gtt Val	gga Gly	aca Thr	atc Ile 350	1059
aaa Lys	tca Ser	tto Phe	ttt Phe	gat Asp 355	Ala	aac Asr	ttg Lev	g gco	cto Leu 360	Thr	gag Glu	g cag n Glr	cct Pro	Ser 365	aag Lys	1107

													ccc Pro 380			1155
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gga Gly 415	gtc Val	tgc Cys	tca Ser	cgt Arg	gtc Val 420	agc Ser	tct Ser	gga Gly	tgt Cys	gaa Glu 425	ctc Leu	aag Lys	gac Asp	tcc Ser	gtg Val 430	1299
atg Met	atg Met	gga Gly	gcg Ala	gac Asp 435	atc Ile	tat Tyr	gaa Glu	act Thr	gaa Glu 440	gaa Glu	gaa Glu	gct Ala	tca Ser	aag Lys 445	cta Leu	1347
													aca Thr 460			1395
													aac Asn			1443
atc Ile	aca Thr 480	aac Asn	agt Ser	aag Lys	Gly	atc Ile 485	caa Gln	gag Glu	gct Ala	gat Asp	cac His 490	Pro	gaa Glu	gaa Glu	gjà aaa	1491
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				gtc Val 515	Ile		atcg	gct	gcgt	ktgc	g					1576

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<211> 516

<212> PRT

<213> Zea mays

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

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36

50 55 60 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 70 75 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 120 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 135 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 150 155 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 185 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 200 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 215 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 230 235 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 250 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 280 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 295 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 345 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355

37

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 375 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His 390 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 410 405 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 420 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu 440 Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 21 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (321) <223> n = a or g or c or t/u, unknown, or other. <220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation

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<222> (1368) $\langle 223 \rangle$ r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1578) <223> k = g or t.<400> 21 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala 50 55 tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 70 65 get gat gea aac egt gta tet gek ate att ttg gge gga gge aet gga 291 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly 85 tot cag etc ttt cet etg aca age aca acn get acg ect get gta ect 339 Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro 100 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 120 115 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr teg ett aac ege eat att eat egt aca tac ett gaa gge ggg ate aac 483 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 180

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att

38

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Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 475 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 23 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1368) <223> r = a or g; amino acid 453 = Pro. <220> <221> variation <222> (1389) <223> h = a or c or t/u.<220> <221> variation <222> (1578) <223> k = g or t.<400> 23 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His 1 cag ata aga tot tgt gag ggt gat ggg att gac agg ttg gaa aaa tta Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu 25 20

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Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

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Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 435 440 445

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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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tac Tyr 495	Туг	ata Ile	agg Arg	tct Ser	gga Gly 500	, Ile	gtg Val	g gtg Val	ato . Ile	cto Lev 505	і Гу	g aat s Asr	gca Ala	aco Thr	atc Ile 510	1539
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<212> PRT

<213> Zea mays

<400> 26

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Gly	Gly	Arg 35	Lys	Gln	Glu	ГÀЗ	Ala 40	Leu	Arg	Asn	Arg	Cys 45	Phe	Gly	Gly
Arg	Val 50	Ala	Ala	Thr	Thr `	Gln 55	Сув	Ile	Leu	Thr	Ser 60	Asp	Ala	Cys	Pro
Glu 65	Thr	Leu	His	Ser	Gln 70	Thr	Gln	Ser	Ser	Arg 75	Lys	Asn	Tyr	Ala	Asp 80
Ala	Asn	Arg	Val	Ser 85	Ala	Ile	Ile	Leu	Gly 90	Gly	Gly	Thr	Gly	Ser 95	Gln
Leu	Phe	Pro	Leu 100	Thr	Ser	Thr	Arg	Ala 105	Thr	Pro	Ala	Val	Pro 110	Val	Gly
Gly	Cya	Tyr 115	Arg	Leu	Ile	Asp	Ile 120	Pro	Met	Ser	Asn	Cys 125	Phe	Asn	Ser
Gly	Ile 130	Asn	Lys	Ile	Phe	Val 135	Met	Ser	Gln	Phe	Asn 140	Ser	Thr	Ser	Leu
Asn 145	Arg	His	Ile	His	Arg 150	Thr	Tyr	Leu	Glu	Gly 155	Gly	Ile	Asn	Phe	Ala 160
Asp	Gly	Ser	Val	Gln 165	Val	Leu	Ala	Ala	Thr 170	Gln	Met	Pro	Glu	Glu 175	Pro
Ala	Gly	Trp	Phe 180		Gly	Thr	Ala	Asp 185	Ser	,Ile	Arg	Lys	Phe 190	Ile	Trp
Val	Leu	Glu 195		Tyr	Tyr	Ser	His 200	Lys	Ser	Ile	Asp	Asn 205		Val	Ile
Leu	Ser 210		Asp	Gln	Leu	Tyr 215	Pro	Met	Asn	Tyr	Met 220	Glu	Leu	Val	Gln
Lys 225		Val	Glu	Asp	Asp 230	Ala	Asp	Ile	Thr	Ile 235		Сув	Ala	Pro	Val 240
Asp	Glu	Ser	Arg	Ala 245		Lys	Asn	Gly	Leu 250		Lys	Ile	Asp	His 255	Thr
Gly	Arg	Val	Leu 260		Phe	Phe	Glu	Lys 265		Lys	Gly	Ala	270		Asn
Ser	Met	275		. Glu	Thr	Asn	Phe 280		Ser	Tyr	Ala	11e 285		Asp	Ala
Glr	Lys 290		Pro	туг	Leu	Ala 295		Met	: Gly	Ile	300		. Ph∈	е Ьув	Lys
Asp 305		Lev	ı Lev	ı Asp	Leu 310		Lys	Ser	. PAS	315		Glr	ı Lev	ı His	320
			- ~7-	1-		n	7 ~~	. א ז -	. T727	T.O.	λer	Tree	- 001	- 17a1	Gln

51 335 325 330 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 360 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp 395 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met 425 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu 440 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 470 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 485 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 27 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS · <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) <223> k = g or t; amino acid 86 = Ala. <220>

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<222> (1287)
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<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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                          85
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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
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gag Glu 175	cca Pro	gtn Val	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
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											aat Asn					675
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cct Pro	gtt Val 240	gat Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	tct Ser	aaa Lys	aat Asn	gjy aaa	cta Leu 250	gtg Val	aag Lys	att Ile	gat Asp	771
cat His 255	act Thr	gga Gly	cgt Arg	gta Val	ctt Leu 260	caa Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	cca Pro	aag Lys	ggt	gct Ala	gat Asp 270	819
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cat His	gac Asp 320	Phe	gga Gly	tct Ser	gaa Glu	ato Ile 325	Leu	cca Pro	aga Arg	gct Ala	gta Val 330	. Lev	gat Asp	cay His	agt Ser	1011
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 75 70 65

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- Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125
- Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu 130 135 140
- Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala 145 150 155 160
- Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro 165 170 175
- Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190
- Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205
- Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220
- Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240
- Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255
- Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn 260 265 270
- Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala 275 280 285
- Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys 290 295 300
- Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp 305 310 315 320
- Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln 325 330 335
- Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser 340 345 350
- Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365
- Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380
- Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp

56

400 390 395 385 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 440 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 455 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 475 470 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 490 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 505 Gly Ser Val Ile 515 <210> 29 <211> 1576 <212> DNA <213> Zea mays <220> <221> CDS <222> (10)..(1563) <223> Shrunken-2 gene revertant form, modified to be heat stable <220> <221> variation <222> (267) $\langle 223 \rangle$ k = g or t; amino acid 86 = Ala. <220> <221> variation <222> (981) <223> r = g or a.<220> <221> variation <222> (1008) <223> y = c or t.<220> <221> variation <222> (1086) <223> n = a or g or c or t/u, unknown, or other. <220>

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<223> r = a or g; amino acid 453 = Pro.
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
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tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
                                                                    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
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gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
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15

ì

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WO 2005/019425

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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80

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Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr 245 250 255

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84

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Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380

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Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp 500 505 510

Gly Ser Val Ile 515

<210> 41

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>

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<221> variation
<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.
<220>
<221> variation
<222> (1008)
<223> y = c or t.
<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.
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<221> variation
<222> (1368)
<223> r = a \text{ or } g; \text{ amino acid } 453 = Pro.
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<221> variation
<222> (1578)
<223> k = g \text{ or t.}
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          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta
                                                                      99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt
                                                                      147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct
                                                                      195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga
                                                                      291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct
                                                                      339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95
                     100
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gtt Val	gga Gly	gga Gly	tgt Cys	tac Tyr 115	agg Arg	ctt Leu	att Ile	gat Asp	atc Ile 120	cct Pro	atg Met	agt Ser	aac Asn	tgc Cys 125	ttc Phe	387
aac Asn	agt Ser	ggt Gly	ata Ile 130	aat Asn	aag Lys	ata Ile	ttt Phe	gtg Val 135	atg Met	agt Ser	cag Gln	ttc Phe	aat Asn 140	tct Ser	act Thr	435
tcg Ser	ctt Leu	aac Asn 145	cgc Arg	cat His	att Ile	cat His	cgt Arg 150	aca Thr	tac Tyr	ctt Leu	gaa Glu	ggc Gly 155	gjà aaa	atc Ile	aac Asn	483
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gag Glu 175	cca Pro	gtn Val	gga Gly	tgg Trp	ttc Phe 180	cag Gln	ggt Gly	aca Thr	gca Ala	gac Asp 185	tct Ser	atc Ile	aga Arg	aaa Lys	ttt Phe 190	579
atc Ile	tgg Trp	gta Val	ctc Leu	gag Glu 195	gat Asp	tat Tyr	tac Tyr	agt Ser	cac His 200	aaa Lys	tcc Ser	att Ile	gac Asp	aac Asn 205	att Ile	627
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gtg Val	cag Gln	aaa Lys 225	His	gtc Val	gag Glu	gac Asp	ģat Asp 230	Ala	gat Asp	atc Ile	act Thr	ata Ile 235	Ser	tgt Cys	gct Ala	723
cct Pro	gtt Val 240	Asp	gag Glu	agc Ser	cga Arg	gct Ala 245	Ser	aaa Lys	aat Asn	Gly 999	cta Leu 250	Val	aag Lys	att Ile	gat Asp	771
cat His 255	Thr	gga Gly	. cgt . Arg	gta Val	ctt Leu 260	Gln	ttc Phe	ttt Phe	gaa Glu	aaa Lys 265	Pro	aag Lys	ggt Gly	gct Ala	gat Asp 270	819
ttg Leu	aat Asn	tct Ser	atg Met	aga Arg 275	Val	gag Glu	aco Thr	aac Asn	tto Phe 280	Lev	ago Ser	tat Tyr	gct Ala	ata Ile 285	gat Asp	867
gat Asp	gca Ala	cag Glr	д ааа 1 Б уя 290	тут	cca Pro	tac Tyr	ctt Leu	gca Ala 295	Ser	ato Met	: Gl ⁷ a aad	att / Ile	tat Tyr 300	· Val	ttc Phe	915
aag Lys	g aaa B Lys	a gat B Asp 305	Ala	a Ctt	tta Lev	gac As <u>r</u>	tetto Let 310	ı Lev	aag Lys	g tca s Sen	a aaa c Lys	a tat s Tyr 319	Thi	caa Glr	tta Leu	963
cat His	gad B Asp 320	Phe	gga Gly	a tct / Sei	gaa Glu	ato Ile 325	e Let	c cca	a aga o Arg	a gci g Ala	gta Val 33	l Lei	a gat ı Ası	tay Tyi	y agt c Ser	1011
gtg Val 335	l Gli	g gca n Ala	a tgo a Cyn	c att	ttt Phe	Th	g ggo c Gl	c tai	t tgg r Trj	g gag p Gli 34	ı Ası	t gti p Vai	gg:	a aca y Thi	a atc r Ile 350	1059

aaa Lys	tca Ser	ttc Phe	ttt Phe	gat Asp 355	gca Ala	aac Asn	ttg Leu	gcc Ala	ctc Leu 360	act Thr	gag Glu	cag Gln	cct Pro	tcc Ser 365	aag Lys	1107
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tac Tyr 495	Tyr	ata Ile	agg Arg	tct Ser	gga Gly 500	Ile	gtg Val	gtg Val	ato	ctg Lev 505	r	aat Asn	gca Ala	acc Thr	atc Ile 510	1539
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<400> 42

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88

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89

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp 355 360 365

- Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro 370 375 380
- Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp 385 390 395 400
- Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val 405 410 415
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- Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu 435 440 445
- Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn 450 455 460
- Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr 465 470 475 480
- Asn Ser Lys Gly Ile Glu Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr 485 490 495
- Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
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Gly Ser Val Ile 515